



IFWO

## RAW SEQUENCE LISTING

DATE: 10/07/2004

PATENT APPLICATION: US/10/726,198

TIME: 13:53:35

Input Set : A:\mandalmed 11.ST25.txt

Output Set: N:\CRF4\10072004\J726198.raw

3 <110> APPLICANT: John, Constance M.  
 4       Jarvis, Gary A.  
 5       Leffler, Hakon  
 7 <120> TITLE OF INVENTION: SUSTAINED RELEASE N-TERMINALLY TRUNCATED GALECTIN-3 AND  
 8       ANTIBODIES TO GALECTIN-3 CARBOHYDRATE LIGANDS FOR USE IN TREATING  
 9       DISEASE  
 11 <130> FILE REFERENCE: 3157.00011  
 13 <140> CURRENT APPLICATION NUMBER: 10/726,198  
 14 <141> CURRENT FILING DATE: 2003-12-02  
 16 <150> PRIOR APPLICATION NUMBER: 60/430,253  
 17 <151> PRIOR FILING DATE: 2002-12-02  
 19 <150> PRIOR APPLICATION NUMBER: PCT/US02/18478  
 20 <151> PRIOR FILING DATE: 2002-06-10  
 22 <160> NUMBER OF SEQ ID NOS: 15  
 24 <170> SOFTWARE: PatentIn version 3.2  
 26 <210> SEQ ID NO: 1  
 27 <211> LENGTH: 143  
 28 <212> TYPE: PRT  
 29 <213> ORGANISM: homo sapien  
 31 <400> SEQUENCE: 1  
 33 Gly Ala Pro Ala Gly Pro Leu Ile Val Pro Tyr Asn Leu Pro Leu Pro  
 34 1                               5                               10                               15  
 37 Gly Gly Val Val Pro Arg Met Leu Ile Thr Ile Leu Gly Thr Val Lys  
 38                               20                               25                               30  
 41 Pro Asn Ala Asn Arg Ile Ala Leu Asp Phe Gln Arg Gly Asn Asp Val  
 42                               35                               40                               45  
 45 Ala Phe His Phe Asn Pro Arg Phe Asn Glu Asn Asn Arg Arg Val Ile  
 46                               50                               55                               60  
 49 Val Cys Asn Thr Lys Leu Asp Asn Asn Trp Gly Arg Glu Glu Arg Gln  
 50 65                               70                               75                               80  
 53 Ser Val Phe Pro Phe Glu Ser Gly Lys Pro Phe Lys Ile Gln Val Leu  
 54                               85                               90                               95  
 57 Val Glu Pro Asp His Phe Lys Val Ala Val Asn Asp Ala His Leu Leu  
 58                               100                               105                               110  
 61 Gln Tyr Asn His Arg Val Lys Lys Leu Asn Glu Ile Ser Lys Leu Gly  
 62                               115                               120                               125  
 65 Ile Ser Gly Asp Ile Asp Leu Thr Ser Ala Ser Tyr Thr Met Ile  
 66                               130                               135                               140  
 69 <210> SEQ ID NO: 2  
 70 <211> LENGTH: 144  
 71 <212> TYPE: PRT  
 72 <213> ORGANISM: homo sapien  
 74 <400> SEQUENCE: 2



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76 Cys Gly Ala Pro Ala Gly Pro Leu Ile Val Pro Tyr Asn Leu Pro Leu
77 1 5 10 15
80 Pro Gly Gly Val Val Pro Arg Met Leu Ile Thr Ile Leu Gly Thr Val
81 20 25 30
84 Lys Pro Asn Ala Asn Arg Ile Ala Leu Asp Phe Gln Arg Gly Asn Asp
85 35 40 45
88 Val Ala Phe His Phe Asn Pro Arg Phe Asn Glu Asn Asn Arg Arg Val
89 50 55 60
92 Ile Val Cys Asn Thr Lys Leu Asp Asn Asn Trp Gly Arg Glu Glu Arg
93 65 70 75 80
96 Gln Ser Val Phe Pro Phe Glu Ser Gly Lys Pro Phe Lys Ile Gln Val
97 85 90 95
100 Leu Val Glu Pro Asp His Phe Lys Val Ala Val Asn Asp Ala His Leu
101 100 105 110
104 Leu Gln Tyr Asn His Arg Val Lys Lys Leu Asn Glu Ile Ser Lys Leu
105 115 120 125
108 Gly Ile Ser Gly Asp Ile Asp Leu Thr Ser Ala Ser Tyr Thr Met Ile
109 130 135 140
112 <210> SEQ ID NO: 3
113 <211> LENGTH: 250
114 <212> TYPE: PRT
115 <213> ORGANISM: homo sapien
117 <400> SEQUENCE: 3
119 Met Ala Asp Asn Phe Ser Leu His Asp Ala Leu Ser Gly Ser Gly Asn
120 1 5 10 15
123 Pro Asn Pro Gln Gly Trp Pro Gly Ala Trp Gly Asn Gln Pro Ala Gly
124 20 25 30
127 Ala Gly Gly Tyr Pro Gly Ala Ser Tyr Pro Gly Ala Tyr Pro Gly Gln
128 35 40 45
131 Ala Pro Pro Gly Ala Tyr Pro Gly Gln Ala Pro Pro Gly Ala Tyr His
132 50 55 60
135 Gly Ala Pro Gly Ala Tyr Pro Gly Ala Pro Ala Pro Gly Val Tyr Pro
136 65 70 75 80
139 Gly Pro Pro Ser Gly Pro Gly Ala Tyr Pro Ser Ser Gly Gln Pro Ser
140 85 90 95
143 Ala Pro Gly Ala Tyr Pro Ala Thr Gly Pro Tyr Gly Ala Pro Ala Gly
144 100 105 110
147 Pro Leu Ile Val Pro Tyr Asn Leu Pro Leu Pro Gly Gly Val Val Pro
148 115 120 125
151 Arg Met Leu Ile Thr Ile Leu Gly Thr Val Lys Pro Asn Ala Asn Arg
152 130 135 140
155 Ile Ala Leu Asp Phe Gln Arg Gly Asn Asp Val Ala Phe His Phe Asn
156 145 150 155 160
159 Pro Arg Phe Asn Glu Asn Asn Arg Arg Val Ile Val Cys Asn Thr Lys
160 165 170 175
163 Leu Asp Asn Asn Trp Gly Arg Glu Glu Arg Gln Ser Val Phe Pro Phe
164 180 185 190
167 Glu Ser Gly Lys Pro Phe Lys Ile Gln Val Leu Val Glu Pro Asp His
168 195 200 205

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171 Phe Lys Val Ala Val Asn Asp Ala His Leu Leu Gln Tyr Asn His Arg
172      210                      215                      220
175 Val Lys Lys Leu Asn Glu Ile Ser Lys Leu Gly Ile Ser Gly Asp Ile
176 225                      230                      235                      240
179 Asp Leu Thr Ser Ala Ser Tyr Thr Met Ile
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184 <211> LENGTH: 143
185 <212> TYPE: PRT
186 <213> ORGANISM: homo sapien
188 <400> SEQUENCE: 4
190 Gly Ala Pro Ala Gly Pro Leu Ile Val Pro Tyr Asn Leu Pro Leu Pro
191 1      5      10      15
194 Gly Gly Val Val Pro Arg Met Leu Ile Thr Ile Leu Gly Thr Val Lys
195      20      25      30
198 Pro Asn Ala Asn Arg Ile Ala Leu Asp Phe Gln Arg Gly Asn Asp Val
199      35      40      45
202 Ala Phe His Phe Asn Pro Arg Phe Asn Glu Asn Asn Arg Arg Val Ile
203      50      55      60
206 Val Cys Asn Thr Lys Leu Asp Asn Asn Trp Gly Arg Glu Glu Arg Gln
207 65      70      75      80
210 Ser Val Phe Pro Phe Glu Ser Gly Lys Pro Phe Lys Ile Gln Val Leu
211      85      90      95
214 Val Glu Pro Glu His Phe Lys Val Ala Val Asn Asp Ala His Leu Leu
215      100     105     110
218 Gln Tyr Asn His Arg Val Lys Lys Leu Asn Glu Ile Ser Lys Leu Gly
219      115     120     125
222 Ile Ser Gly Asp Ile Asp Leu Thr Ser Ala Ser Tyr Thr Met Ile
223      130     135     140
226 <210> SEQ ID NO: 5
227 <211> LENGTH: 143
228 <212> TYPE: PRT
229 <213> ORGANISM: homo sapien
231 <400> SEQUENCE: 5
233 Gly Ala Pro Ala Gly Pro Leu Ile Val Pro Tyr Asn Leu Pro Leu Pro
234 1      5      10      15
237 Gly Gly Val Val Pro Arg Met Leu Ile Thr Ile Leu Gly Thr Val Lys
238      20      25      30
241 Pro Asn Ala Asn Arg Ile Ala Leu Asp Phe Gln Arg Gly Asn Asp Val
242      35      40      45
245 Ala Phe His Phe Asn Pro Arg Phe Asn Glu Asn Asn Arg Arg Val Ile
246      50      55      60
249 Val Cys Asn Thr Lys Leu Asp Asn Asn Trp Gly Arg Glu Glu Arg Gln
250 65      70      75      80
253 Ser Val Phe Pro Phe Glu Ser Gly Lys Pro Phe Lys Ile Gln Val Leu
254      85      90      95
257 Val Glu Pro Glu His Phe Lys Val Ala Val Asn Asp Ala His Leu Leu
258      100     105     110
261 Gln Tyr Asn His Arg Ala Lys Lys Leu Asn Glu Ile Ser Lys Leu Gly

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262          115          120          125
265 Ile Ser Gly Asp Ile Asp Leu Thr Ser Ala Ser Tyr Thr Met Ile
266          130          135          140
269 <210> SEQ ID NO: 6
270 <211> LENGTH: 27
271 <212> TYPE: DNA
272 <213> ORGANISM: artificial sequence
274 <220> FEATURE:
275 <223> OTHER INFORMATION: primer
278 <220> FEATURE:
279 <221> NAME/KEY: misc_feature
280 <222> LOCATION: (1)..(27)
281 <223> OTHER INFORMATION: primer
283 <400> SEQUENCE: 6
284 gacgacgaca agggcgcccc tgctggg                27
287 <210> SEQ ID NO: 7
288 <211> LENGTH: 30
289 <212> TYPE: DNA
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292 <220> FEATURE:
293 <223> OTHER INFORMATION: primer
296 <220> FEATURE:
297 <221> NAME/KEY: misc_feature
298 <222> LOCATION: (1)..(30)
299 <223> OTHER INFORMATION: primer
301 <400> SEQUENCE: 7
302 gaggagaagc ccggtttata tcatggtata                30
305 <210> SEQ ID NO: 8
306 <211> LENGTH: 30
307 <212> TYPE: DNA
308 <213> ORGANISM: artificial sequence
310 <220> FEATURE:
311 <223> OTHER INFORMATION: primer
314 <220> FEATURE:
315 <221> NAME/KEY: misc_feature
316 <222> LOCATION: (1)..(30)
317 <223> OTHER INFORMATION: primer
319 <400> SEQUENCE: 8
320 gacgacgaca agtgcgggcg ccctgctggg                30
323 <210> SEQ ID NO: 9
324 <211> LENGTH: 30
325 <212> TYPE: DNA
326 <213> ORGANISM: artificial sequence
328 <220> FEATURE:
329 <223> OTHER INFORMATION: primer
332 <220> FEATURE:
333 <221> NAME/KEY: misc_feature
334 <222> LOCATION: (1)..(30)
335 <223> OTHER INFORMATION: primer

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337 <400> SEQUENCE: 9
338 gaggagaagc ccggtttata tcatggtata 30
341 <210> SEQ ID NO: 10
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343 <212> TYPE: DNA
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346 <220> FEATURE:
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351 <221> NAME/KEY: misc_feature
352 <222> LOCATION: (1)..(36)
353 <223> OTHER INFORMATION: primer
355 <400> SEQUENCE: 10
356 gacgacgaca agtgcggcgc ccctgctggg ccactg 36
359 <210> SEQ ID NO: 11
360 <211> LENGTH: 27
361 <212> TYPE: DNA
362 <213> ORGANISM: artificial sequence
364 <220> FEATURE:
365 <223> OTHER INFORMATION: primer
368 <220> FEATURE:
369 <221> NAME/KEY: misc_feature
370 <222> LOCATION: (1)..(27)
371 <223> OTHER INFORMATION: primer
373 <400> SEQUENCE: 11
374 actggtgaac ctgaacactt caaggtt 27
377 <210> SEQ ID NO: 12
378 <211> LENGTH: 27
379 <212> TYPE: DNA
380 <213> ORGANISM: artificial sequence
382 <220> FEATURE:
383 <223> OTHER INFORMATION: primer
386 <220> FEATURE:
387 <221> NAME/KEY: misc_feature
388 <222> LOCATION: (1)..(27)
389 <223> OTHER INFORMATION: primer
391 <400> SEQUENCE: 12
392 aaccttgaag tggttcagggtt caacact 27
395 <210> SEQ ID NO: 13
396 <211> LENGTH: 27
397 <212> TYPE: DNA
398 <213> ORGANISM: artificial sequence
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**VERIFICATION SUMMARY**

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